

SEQUENCE LISTING

<110> Brenda F. Baker
Susan M. Freier
Andrew T. Watt

<120> ANTISENSE MODULATION OF UROKINASE PLASMINOGEN ACTIVATOR EXPRESSION

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<223> Antisense Oligonucleotide

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<223> Antisense Oligonucleotide

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<213> Homo sapiens

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<222> (77)...(1372)

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Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val

1

5

10

ctg gtc gtg agc gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca 160

Leu Val Val Ser Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro

15

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25

tcg aac tgt gac tgt cta aat gga gga aca tgt gtg tcc aac aag tac 208

Ser Asn Cys Asp Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr

30

35

40

ttc tcc aac att cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag 256

Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln

45

50

55

60

cac tgt gaa ata gat aag tca aaa acc tgc tat gag ggg aat ggt cac	304
His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His	
65 70 75	
ttt tac cga gga aag gcc agc act gac acc atg ggc cgg ccc tgc ctg	352
Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu	
80 85 90	
ccc tgg aac tct gcc act gtc ctt cag caa acg tac cat gcc cac aga	400
Pro Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg	
95 100 105	
tct gat gct ctt cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac	448
Ser Asp Ala Leu Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn	
110 115 120	
cca gac aac cgg agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag	496
Pro Asp Asn Arg Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys	
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Pro Leu Val Gln Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys	
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ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag act	592
Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr	
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ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc gag	640
Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu	
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aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct	688
Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser	
190 195 200	

gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc 736
Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile
205 210 215 220

agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac atc 784
Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile
225 230 235

gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag atg 832
Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met
240 245 250

aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct gac 880
Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp
255 260 265

acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc aag 928
Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys
270 275 280

gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc ctg 976
Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu
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Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr
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Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu
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aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag ccc 1120
Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro
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 His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp
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 Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly
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<400> 4

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23

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<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 5

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<212> DNA

<213> Artificial Sequence

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<223> PCR Probe

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24

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<223> PCR Primer

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<223> PCR Probe

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Met Lys Val Trp Leu Ala Ser Leu Phe Leu Cys Ala Leu Val Val Lys
1 5 10 15

aac tct gaa ggt ggc agt gta ctt gga gct cct gat gaa tca aac'tgt 154
Asn Ser Glu Gly Gly Ser Val Leu Gly Ala Pro Asp Glu Ser Asn Cys
20 25 30

ggc tgt cag aac gga ggt gta tgc gtg tcc tac aag tac ttc tcc aga 202
Gly Cys Gln Asn Gly Gly Val Cys Val Ser Tyr Lys Tyr Phe Ser Arg
35 40 45

att cgc cga tgc agc tgc cca agg aaa ttc cag ggg gag cac tgt gag 250
Ile Arg Arg Cys Ser Cys Pro Arg Lys Phe Gln Gly Glu His Cys Glu
50 55 60

ata gat gca tca aaa acc tgc tat cat gga aat ggt gac tct tac cga 298
Ile Asp Ala Ser Lys Thr Cys Tyr His Gly Asn Gly Asp Ser Tyr Arg
65 70 75 80

gga aag gcc aac act gat acc aaa ggt cgg ccc tgc ctg gcc tgg aat 346
Gly Lys Ala Asn Thr Asp Thr Lys Gly Arg Pro Cys Leu Ala Trp Asn
85 90 95

gcg cct gct gtc ctt cag aaa ccc tac aat gcc cac aga cct gat gct 394
Ala Pro Ala Val Leu Gln Lys Pro Tyr Asn Ala His Arg Pro Asp Ala
100 105 110

att agc cta ggc ctg ggg aaa cac aat tac tgc agg aac cct gac aac 442
Ile Ser Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn

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Gln Lys Arg Pro Trp Cys Tyr Val Gln Ile Gly Leu Arg Gln Phe Val			
130	135	140	
caa gaa tgc atg gtg cat gac tgc tct ctt agc aaa aag cct tct tcg			538
Gln Glu Cys Met Val His Asp Cys Ser Leu Ser Lys Lys Pro Ser Ser			
145	150	155	160
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Ser Val Asp Gln Gln Gly Phe Gln Cys Gly Gln Lys Ala Leu Arg Pro			
165	170	175	
cgc ttt aag att gtt ggg gga gaa ttc act gag gtg gag aac cag ccc			634
Arg Phe Lys Ile Val Gly Gly Glu Phe Thr Glu Val Glu Asn Gln Pro			
180	185	190	
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Trp Phe Ala Ala Ile Tyr Gln Lys Asn Lys Gly Gly Ser Pro Pro Ser			
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Phe Lys Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ala Ser Ala			
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gca cac tgc ttc att caa ctc cca aag aag gaa aac tac gtt gtc tac			778
Ala His Cys Phe Ile Gln Leu Pro Lys Lys Glu Asn Tyr Val Val Tyr			
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ctg ggt cag tcg aag gag agc tcc tat aat cct gga gag atg aag ttt			826
Leu Gly Gln Ser Lys Glu Ser Ser Tyr Asn Pro Gly Glu Met Lys Phe			
245	250	255	
gag gtg gag cag ctc atc ttg cac gaa tac tac agg gaa gac agc ctg			874
Glu Val Glu Gln Leu Ile Leu His Glu Tyr Tyr Arg Glu Asp Ser Leu			

260	265	270	
gcc tac cat aat gat att gcc ttg ctg aag ata cgt acc agc acg ggc			922
Ala Tyr His Asn Asp Ile Ala Leu Leu Lys Ile Arg Thr Ser Thr Gly			
275	280	285	
caa tgt gca cag cca tcc agg tcc ata cag acc atc tgc ctg ccc cca			970
Gln Cys Ala Gln Pro Ser Arg Ser Ile Gln Thr Ile Cys Leu Pro Pro			
290	295	300	
agg ttt act gat gct ccg ttt ggt tca gac tgt gag atc act ggc ttt			1018
Arg Phe Thr Asp Ala Pro Phe Gly Ser Asp Cys Glu Ile Thr Gly Phe			
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Gly Lys Glu Ser Glu Ser Asp Tyr Leu Tyr Pro Lys Asn Leu Lys Met			
325	330	335	
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Ser Val Val Lys Leu Val Ser His Glu Gln Cys Met Gln Pro His Tyr			
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tat ggc tct gaa att aat tat aaa atg ctg tgt gct gcg gac cca gag			1162
Tyr Gly Ser Glu Ile Asn Tyr Lys Met Leu Cys Ala Ala Asp Pro Glu			
355	360	365	
tgg aaa aca gat tcc tgc aag ggc gat tct gga gga ccg ctt atc tgt			1210
Trp Lys Thr Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Ile Cys			
370	375	380	
aac atc gaa ggc cgc cca act ctg agt ggg att gtg agc tgg ggc cga			1258
Asn Ile Glu Gly Arg Pro Thr Leu Ser Gly Ile Val Ser Trp Gly Arg			
385	390	395	400
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Gly Cys Ala Glu Lys Asn Lys Pro Gly Val Tyr Thr Arg Val Ser His			

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Phe Leu Asp Trp Ile Gln Ser His Ile Gly Glu Glu Lys Gly Leu Ala			
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<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 11

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<223> PCR Primer

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<210> 13

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<212> DNA

<213> Artificial Sequence

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<223> PCR Probe

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22

tgctgtctag agcccagcgg ca

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<211> 27

<212> DNA

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<223> PCR Probe

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27

<210> 17

<211> 7258

<212> DNA

<213> Homo sapiens

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